Amendments to the Specification:

Please replace paragraph beginning on page 8, line 4, with the following amended paragraph:

--Figure 1 shows two mechanisms for Interaction-dependent Enzyme Activation (IdEA). Figure 1A. Ligand-dependent circular permutations of an enzyme are formed by linking the native termini ~~into an "α–ω" domain~~, and severing the polypeptide chain in a solvent exposed loop ~~the "μ" domain~~ to generate new carboxy and amino termini~~μ1 and μ2 subdomains~~. The circularly permutated enzyme can ~~μ1 and μ2~~ refold to form an active enzyme when and only when the new termini ~~they~~ are brought together by an ~~interactionof~~ interaction of heterologous domains fused to the new ~~their~~ termini. The interaction can be direct or mediated by a second molecule (the ligand). The ligand-binding domains can include but are not limited to single-chain antibody fragments (scFv) and constrained peptides scaffolded on a carrier protein (csp). Versatile hydrolytic enzymes such as β-lactamases can be used to confer multiple selectable phenotypes including antibiotic resistance, color, death (prodrug, for inhibitor screens), and auxotrophic growth. Figure 1B. Interaction-dependent fragment complementation requires enzyme α and ω fragments which can reform to form active enzyme when and only when they are brought together by an interaction of heterologous domains fused to their termini.--